

Sequence Listing

<110> ASHKENAZI, AVI J
 BOTSTEIN, DAVID
 DODGE, KELLY H.
 GURNEY, AUSTIN L.
 KIM, KYUNG JIN
 LAWRENCE, DAVID A.
 PITTI, ROBERT
 ROY, MARGARET A
 TUMAS, DANIEL B
 WOOD, WILLIAM I.

<120> DcR3 Polypeptide, A TNFR Homolog

<130> P1134R2 REVISED

<140> US 09/157,289

<141> 1998-09-18

<150> US 60/059,288

<151> 1997-09-18

<150> US 60/094,640

<151> 1998-07-30

<160> 18

<210> 1

<211> 300

<212> PRT

<213> Homo sapiens

<400> 1

Met	Arg	Ala	Leu	Glu	Gly	Pro	Gly	Leu	Ser	Leu	Leu	Cys	Leu	Val
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Leu	Ala	Leu	Pro	Ala	Leu	Leu	Pro	Val	Pro	Ala	Val	Arg	Gly	Val
			20						25					30

Ala	Glu	Thr	Pro	Thr	Tyr	Pro	Trp	Arg	Asp	Ala	Glu	Thr	Gly	Glu
			35						40					45

Arg	Leu	Val	Cys	Ala	Gln	Cys	Pro	Pro	Gly	Thr	Phe	Val	Gln	Arg
			50						55					60

Pro	Cys	Arg	Arg	Asp	Ser	Pro	Thr	Thr	Cys	Gly	Pro	Cys	Pro	Pro
			65						70					75

Arg	His	Tyr	Thr	Gln	Phe	Trp	Asn	Tyr	Leu	Glu	Arg	Cys	Arg	Tyr
			80						85					90

Cys	Asn	Val	Leu	Cys	Gly	Glu	Arg	Glu	Glu	Glu	Ala	Arg	Ala	Cys	95	100	105
His	Ala	Thr	His	Asn	Arg	Ala	Cys	Arg	Cys	Arg	Thr	Gly	Phe	Phe	110	115	120
Ala	His	Ala	Gly	Phe	Cys	Leu	Glu	His	Ala	Ser	Cys	Pro	Pro	Gly	125	130	135
Ala	Gly	Val	Ile	Ala	Pro	Gly	Thr	Pro	Ser	Gln	Asn	Thr	Gln	Cys	140	145	150
Gln	Pro	Cys	Pro	Pro	Gly	Thr	Phe	Ser	Ala	Ser	Ser	Ser	Ser	Ser	155	160	165
Glu	Gln	Cys	Gln	Pro	His	Arg	Asn	Cys	Thr	Ala	Leu	Gly	Leu	Ala	170	175	180
Leu	Asn	Val	Pro	Gly	Ser	Ser	Ser	His	Asp	Thr	Leu	Cys	Thr	Ser	185	190	195
Cys	Thr	Gly	Phe	Pro	Leu	Ser	Thr	Arg	Val	Pro	Gly	Ala	Glu	Glu	200	205	210
Cys	Glu	Arg	Ala	Val	Ile	Asp	Phe	Val	Ala	Phe	Gln	Asp	Ile	Ser	215	220	225
Ile	Lys	Arg	Leu	Gln	Arg	Leu	Leu	Gln	Ala	Leu	Glu	Ala	Pro	Glu	230	235	240
Gly	Trp	Gly	Pro	Thr	Pro	Arg	Ala	Gly	Arg	Ala	Ala	Leu	Gln	Leu	245	250	255
Lys	Leu	Arg	Arg	Arg	Leu	Thr	Glu	Leu	Leu	Gly	Ala	Gln	Asp	Gly	260	265	270
Ala	Leu	Leu	Val	Arg	Leu	Leu	Gln	Ala	Leu	Arg	Val	Ala	Arg	Met	275	280	285
Pro	Gly	Leu	Glu	Arg	Ser	Val	Arg	Glu	Arg	Phe	Leu	Pro	Val	His	290	295	300

<210> 2
 <211> 1114
 <212> DNA
 <213> Homo sapiens

<220>
 <221> Unsure
 <222> 1090

<223> Unknown base

<400> 2

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agggtcctgt gtccgcgctg agccgcgctc tccctgctcc agcaaggacc 100
atgagggcgc tggagggggc aggccgtgctg ctgctgtgcc tgggtgttggc 150
gctgcctgcc ctgctgccgg tgccggctgt acgcggagtg gcagaaacac 200
ccacctaccc ctggcgggac gcagagacag gggagcggct ggtgtgcgcc 250
cagtgcctccc caggcacctt tgtgcagcgg ccgtgccgcc gagacagccc 300
cacgacgtgt ggcccgtgtc caccgcgcca ctacacgcag ttctggaact 350
acctggagcg ctgccgctac tgcaacgtcc tctgcgggga gcgtgaggag 400
gaggcacggg cttgccacgc caccacaac cgtgcctgcc gctgccgcac 450
cggtcttctc gcgcacgctg gtttctgctt ggagcacgca tcgtgtccac 500
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cagccgtgcc ccccaggcac cttctcagcc agcagctcca gctcagagca 600
gtgccagccc caccgcaact gcacggccct gggcctggcc ctcaatgtgc 650
caggctcttc ctcccatgac accctgtgca ccagctgcac tggcttcccc 700
ctcagcacca ggggtaccagg agctgaggag tgtgagcgtg ccgtcatcga 750
ctttgtgggt ttccaggaca tctccatcaa gaggctgcag cggctgctgc 800
aggccctcga ggccccggag ggctggggtc cgacaccaag ggcgggccgc 850
gcggccttgc agctgaagct gcgtcggcgg ctcacggagc tcctgggggc 900
gcaggacggg gcgctgctgg tgccgctgct gcaggcgctg cgctggcca 950
ggatgcccgg gctggagcgg agcgtccgtg agcgttcct ccctgtgcac 1000
tgatcctggc cccctcttat ttattctaca tccttggcac cccacttgca 1050
ctgaaagagg ctttttttta aatagaagaa atgaggttn ttaaaaaaaaa 1100
aaaaaaaaaa aaaa 1114

<210> 3

<211> 491

<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<220>
<221> unsure
<222> 62, 73, 86, 98
<223> unknown base

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gccgagacag cccacgacg tgtggcccg gtccaccg cactacacg 50
cagttctgga antaactgga gcncctgccg tactgnaacg tcctctgngg 100
ggagcgtgag gaggaggcac gggcttgcca cgccaccac aaccgtgect 150
gccgctgccg caccggcttc ttcgcgcacg ctggtttctg cttggagcac 200
gcatcgtgtc cacctggtgc cggcgtgatt gcccgggca cccccagcca 250
gaacacgcag tgcctagccg tgccccccag gcaccttctc agccagcagc 300
tccagctcag agcagtgccg gcccaccgc aactgcaagg ccctgggect 350
ggccctcaat gtgccaggct cttcctccca tgacaccctg tgcaccagct 400
gcactggctt cccctcagc accagggtag caggagctga ggagtgtgag 450
cgtgccgtca tcgactttgt ggctttccag gacatctcca t 491

<210> 4
<211> 73
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<400> 4
gccgagacag cccacgacg tgtggcccg gtccaccg cactacacg 50
cattctggaa ctacctggag cgc 73

<210> 5
<211> 271
<212> DNA
<213> Unknown

<220>

<223> Unknown organism

<220>

<221> unsure

<222> 42, 62, 73, 86, 98, 106, 120, 122, 153, 167, 184, 220, 233

<223> unknown base

<400> 5

gcogagacag ccccaacgacg tgtggcccggt gtccaccgcg cnactacacg 50

cagttctgga antaactgga gncctgccgc tactgnaacg tcctctgngg 100

ggagcntgag gaggaggcan gngcttgcca cgccaccac aaccgcgcct 150

gngctgcag caccggnctt ttgcgcacg ctgntttctg cttggagcac 200

gcacgtgtc cacctggtgn cggcgtgatt gncgcgggca cccccagcca 250

gaacacgcat gcaaagccgt g 271

<210> 6

<211> 201

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<220>

<221> unsure

<222> 182

<223> unknown base

<400> 6

gcagttctgg aactacctgg agcgtgccg ctactgcaac gtcctctgcg 50

gggagcgtga ggaggaggca cgggcttgcc acgccacca caaccgtgcc 100

tgccgctgcc gcaccggctt cttgcgcac gctggtttct gcttgagca 150

cgcacgtgt ccacctggtg ccggcgtgat tncgccggc acccccagcc 200

a 201

<210> 7

<211> 277

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<220>
<221> unsure
<222> 142
<223> unknown base

<400> 7
gaggggcccc caggagtggg ggccggaggt gtggcagggg tcaggttgt 50
ggccccagcc ttgcacctg agctaggaca ccagttcccc tgacctgtt 100
cttccctect ggctgcaggc acccccagcc agaacacgca gnccagccgt 150
gccccccagg caccttctca gccagcagct ccagctcaga gcagtgccag 200
ccccaccgca actgcacggc cctgggcctg gccctcaatg tgccaggctc 250
ttcttcccat gacacctgt gcaccag 277

<210> 8
<211> 199
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<400> 8
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gaacacgcag gcctagccgt gccccccagg caccttctca gccagcagct 100
ccagctcaga gcagtgccag cccccaccgca actgcacggc cctgggcctg 150
gccctcaatg tgccaggctc ttcttcccat gacacctgt gcaccagct 199

<210> 9
<211> 226
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<220>
<221> unsure
<222> 4, 9, 12, 165
<223> unknown base

<400> 9
agcngtgenc cncaggcacc ttctcagcca gcagttccag ctccagagcag 50

tgccagcccc accgcaactg cacggccctg ggccctggccc tcaatgtgcc 100
 aggctcttcc tcccatgaca cgctgtgcac cagctgcact ggcttcccc 150
 tcagcaccag ggtancagga gctgaggagt gtgagcgtgc cgtcatcgac 200
 tttgtggctt tccaggacat ctccat 226

<210> 10
 <211> 283
 <212> DNA
 <213> Homo sapiens

<220>
 <221> Unsure
 <222> 1-283
 <223> Unknown organism

<220>
 <221> unsure
 <222> 27, 64, 140
 <223> unknown base

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 cttgtccacc tgggtgcggc gtgattnccc gggcaccccc agccagaaca 50
 cgcagtgcc a gcntcccc caggcacctt ctcagccagc agctccagct 100
 cagagcagtg ccagccccac cgcaactgca acgccctggn ctggccctca 150
 atgtgccagg ctcttctctc catgacaccc tgtgcaccag ctgcactggc 200
 ttccccctca gcaccagggg accaggagct gaggagtgtg agcgtgccgt 250
 catcgacttt gtggctttcc aggacatctc cat 283

<210> 11
 <211> 21
 <212> DNA
 <213> Unknown

<220>
 <223> Unknown organism

<400> 11
 cacgctgggt tctgcttgga g 21

<210> 12
 <211> 22
 <212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 12

agctggtgca caggggtgtca tg 22

<210> 13

<211> 53

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 13

cccaggcacc ttctcagcca gccagcagct ccagctcaga gcagtgccag 50

ccc 53

<210> 14

<211> 24

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 14

acacgatgcg tgctccaagc agaa 24

<210> 15

<211> 17

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 15

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<210> 16

<211> 16

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 16
 atcacgccgg caccag 16

<210> 17
 <211> 461
 <212> PRT
 <213> Homo sapiens

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 20 25 30
 Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr
 35 40 45
 Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly
 50 55 60
 Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys
 65 70 75
 Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val
 80 85 90
 Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val
 95 100 105
 Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys
 110 115 120
 Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg
 125 130 135
 Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
 140 145 150
 Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala
 155 160 165
 Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg
 170 175 180
 Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser
 185 190 195
 Arg Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala
 200 205 210

Pro Gly Ala Val	His Leu Pro Gln Pro	Val Ser Thr Arg Ser Gln
215	220	225
His Thr Gln Pro	Thr Pro Glu Pro Ser	Thr Ala Pro Ser Thr Ser
230	235	240
Phe Leu Leu Pro	Met Gly Pro Ser Pro	Pro Ala Glu Gly Ser Thr
245	250	255
Gly Asp Phe Ala	Leu Pro Val Gly Leu	Ile Val Gly Val Thr Ala
260	265	270
Leu Gly Leu Leu	Ile Ile Gly Val Val	Asn Cys Val Ile Met Thr
275	280	285
Gln Val Lys Lys	Lys Pro Leu Cys Leu	Gln Arg Glu Ala Lys Val
290	295	300
Pro His Leu Pro	Ala Asp Lys Ala Arg	Gly Thr Gln Gly Pro Glu
305	310	315
Gln Gln His Leu	Leu Ile Thr Ala Pro	Ser Ser Ser Ser Ser Ser
320	325	330
Leu Glu Ser Ser	Ala Ser Ala Leu Asp	Arg Arg Ala Pro Thr Arg
335	340	345
Asn Gln Pro Gln	Ala Pro Gly Val Glu	Ala Ser Gly Ala Gly Glu
350	355	360
Ala Arg Ala Ser	Thr Gly Ser Ser Asp	Ser Ser Pro Gly Gly His
365	370	375
Gly Thr Gln Val	Asn Val Thr Cys Ile	Val Asn Val Cys Ser Ser
380	385	390
Ser Asp His Ser	Ser Gln Cys Ser Ser	Gln Ala Ser Ser Thr Met
395	400	405
Gly Asp Thr Asp	Ser Ser Pro Ser Glu	Ser Pro Lys Asp Glu Gln
410	415	420
Val Pro Phe Ser	Lys Glu Glu Cys Ala	Phe Arg Ser Gln Leu Glu
425	430	435
Thr Pro Glu Thr	Leu Leu Gly Ser Thr	Glu Glu Lys Pro Leu Pro
440	445	450
Leu Gly Val Pro	Asp Ala Gly Met Lys	Pro Ser
455	460	

<210> 18
 <211> 293
 <212> PRT
 <213> Homo sapiens

<400> 18

Met	Asn	Lys	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser
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Ile	Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His
				20					25					30
Tyr	Asp	Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro
				35					40					45
Pro	Gly	Thr	Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr
				50					55					60
Val	Cys	Ala	Pro	Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His
				65					70					75
Thr	Ser	Asp	Glu	Cys	Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu
				80					85					90
Gln	Tyr	Val	Lys	Gln	Glu	Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys
				95					100					105
Glu	Cys	Lys	Glu	Gly	Arg	Tyr	Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys
				110					115					120
His	Arg	Ser	Cys	Pro	Pro	Gly	Phe	Gly	Val	Val	Gln	Ala	Gly	Thr
				125					130					135
Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg	Cys	Pro	Asp	Gly	Phe	Phe
				140					145					150
Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	Arg	Lys	His	Thr	Asn
				155					160					165
Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	Gly	Asn	Ala	Thr
				170					175					180
His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	Gln	Lys	Cys
				185					190					195
Gly	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	Phe	Ala
				200					205					210
Val	Pro	Thr	Lys	Phe	Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	Asp
				215					220					225

Asn	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile
				230					235					240
Lys	Arg	Gln	His	Ser	Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys
				245					250					255
Leu	Trp	Lys	His	Gln	Asn	Lys	Ala	Gln	Asp	Ile	Val	Lys	Lys	Ile
				260					265					270
Ile	Gln	Asp	Ile	Asp	Leu	Cys	Glu	Asn	Ser	Val	Gln	Arg	His	Ile
				275					280					285
Gly	His	Ala	Asn	Leu	Thr	Phe	Glu							
				290										